



## SEQUENCE LISTING

<110> CNRS

<120> STARCH GRANULES CONTAINING A RECOMBINANT POLYPEPTIDE  
OF INTEREST, A METHOD OF OBTAINING THEM AND THEIR  
USES

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<140>

<141>

<150> FR9906494

<151> 1999-05-21

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 3117

<212> DNA

<213> Chlamydomonas reinhardtii

<400> 1

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<210> 2

<211> 2124

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fragment  
of the complete sequence of cDNA coding for the GBSSI  
of *Chlamydomonas reinhardtii*

<220>

<221> CDS

<222> (1)..(2124)

<400> 2

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atc aat gcc gcg tcg ttc ggt gtc aag aag acc gcg aac cag ctg ctg 96
Ile Asn Ala Ala Ser Phe Gly Val Lys Lys Thr Ala Asn Gln Leu Leu
          20             25             30

cgt gag ctt gct cgt ggc tcc gca cgc aag tcc acc tcg cgc tcg gct 144
Arg Glu Leu Ala Arg Gly Ser Ala Arg Lys Ser Thr Ser Arg Ser Ala
      35             40             45

gtt act ggt gcc act ggt gcc act tgc gcg ctg gac atc gtg atg gtt 192
Val Thr Gly Ala Thr Gly Ala Thr Cys Ala Leu Asp Ile Val Met Val
      50             55             60

gct gct gag gtc gcc cct tgg tcc aag acg ggc ggc ctg ggc gat gtg 240
Ala Ala Glu Val Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val
      65             70             75             80

act ggt ggc ctg cct att gag ctg gtc aag cgc ggc cac cgc gtc atg 288
Thr Gly Gly Leu Pro Ile Glu Leu Val Lys Arg Gly His Arg Val Met
          85             90             95

acc att gcc cct cgc tac gac cag tac gct gac gcc tgg gac acc tcg 336
Thr Ile Ala Pro Arg Tyr Asp Gln Tyr Ala Asp Ala Trp Asp Thr Ser
      100             105            110

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gtg gtc gtg gac atc atg ggc gag aag gtc cgc tac ttc cac tcc atc	384
Val Val Val Asp Ile Met Gly Glu Lys Val Arg Tyr Phe His Ser Ile	
115 120 125	
aag aag ggc gtg cac cgc gtg tgg att gac cac ccc tgg ttc ctg gcc	432
Lys Lys Gly Val His Arg Val Trp Ile Asp His Pro Trp Phe Leu Ala	
130 135 140	
aag gtc tgg ggc aag acc ggc tcc aag ctg tac ggc ccc cgc tcc ggc	480
Lys Val Trp Gly Lys Thr Gly Ser Lys Leu Tyr Gly Pro Arg Ser Gly	
145 150 155 160	
gct gac tac ctg gac aac cac aag cgc ttc gcc ctg ttc tgc aag gcc	528
Ala Asp Tyr Leu Asp Asn His Lys Arg Phe Ala Leu Phe Cys Lys Ala	
165 170 175	
gct att gag gct gcc cgc gtg ctg ccc ttc ggc ccc ggc gag gac tgc	576
Ala Ile Glu Ala Ala Arg Val Leu Pro Phe Gly Pro Gly Glu Asp Cys	
180 185 190	
gtc ttc gtg gcc aac gac tgg cac tcc gcc ctg gtg ccc gtc ctg ctg	624
Val Phe Val Ala Asn Asp Trp His Ser Ala Leu Val Pro Val Leu Leu	
195 200 205	
aag gac gag tac cag ccc aag ggc cag ttc acc aag gcc aag tcg gtg	672
Lys Asp Glu Tyr Gln Pro Lys Gly Gln Phe Thr Lys Ala Lys Ser Val	
210 215 220	
ctg gct atc cac aac atc gcc ttc cag ggc cgc atg tgg gag gag gct	720
Leu Ala Ile His Asn Ile Ala Phe Gln Gly Arg Met Trp Glu Glu Ala	
225 230 235 240	
ttc aag gac acg aag ctg ccc cag gcc gcc ttt gac aag ctg gcc ttc	768
Phe Lys Asp Thr Lys Leu Pro Gln Ala Ala Phe Asp Lys Leu Ala Phe	
245 250 255	
tcg gac ggc tat gcc aag gtt tac act gag gcc acc ccc atg gag gag	816
Ser Asp Gly Tyr Ala Lys Val Tyr Thr Glu Ala Thr Pro Met Glu Glu	
260 265 270	
gac gag aag ccc ccg ctg acg gga aag acc tac aag aag atc aac tgg	864
Asp Glu Lys Pro Pro Leu Thr Gly Lys Thr Tyr Lys Lys Ile Asn Trp	
275 280 285	
ctg aag ggt ggc att atc gcc gcc gac aag ctg gtg act gtg tcg ccc	912
Leu Lys Gly Gly Ile Ile Ala Ala Asp Lys Leu Val Thr Val Ser Pro	
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Asn Tyr Ala Thr Glu Ile Ala Ala Asp Ala Ala Gly Gly Val Glu Leu	
305 310 315 320	
gac acc gtc atc cgc gcc aag ggc att gag ggc att gtg aac ggc atg	1008
Asp Thr Val Ile Arg Ala Lys Gly Ile Glu Gly Ile Val Asn Gly Met	
325 330 335	
gac att gag gag tgg aac ccc aag acc gac aag ttc ctg tct gcg ccc	1056
Asp Ile Glu Glu Trp Asn Pro Lys Thr Asp Lys Phe Leu Ser Ala Pro	
340 345 350	

tac gac cag aac agc gtc tac gcc ggc aag gcc gcc gcc aag gag gcc	1104
Tyr Asp Gln Asn Ser Val Tyr Ala Gly Lys Ala Ala Ala Lys Glu Ala	
355 360 365	
ctg cag gcc gag ctg ggc ctg cct gtg gac ccc acc gcc ccc ctg ttc	1152
Leu Gln Ala Glu Leu Gly Leu Pro Val Asp Pro Thr Ala Pro Leu Phe	
370 375 380	
gcc ttc atc ggc cgc ctg gag gag cag aag ggt gtg gac atc atc ctg	1200
Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Val Asp Ile Ile Leu	
385 390 395 400	
gcc gcc ctg ccc aag atc ctg gcc acc ccc aag gtg cag atc gcc atc	1248
Ala Ala Leu Pro Lys Ile Leu Ala Thr Pro Lys Val Gln Ile Ala Ile	
405 410 415	
ctg ggt acc ggc aag gcc gcc tac gag aag ctg gtg aac gcc atc ggc	1296
Leu Gly Thr Gly Lys Ala Ala Tyr Glu Lys Leu Val Asn Ala Ile Gly	
420 425 430	
acc aag tac aag ggc cgc gcc aag ggc gtg gtc aag ttc tcg gcg ccc	1344
Thr Lys Tyr Lys Gly Arg Ala Lys Gly Val Val Lys Phe Ser Ala Pro	
435 440 445	
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Leu Ala His Met Leu Thr Ala Gly Ala Asp Phe Met Leu Val Pro Ser	
450 455 460	
cgc ttc gag ccc tgc ggc ctg atc cag ctg cac gcc atg cac tac ggt	1440
Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu His Ala Met His Tyr Gly	
465 470 475 480	
acc gtg ccc gtg gta gcc tcc acc ggc ggc ctg gtc gac acc gtc aag	1488
Thr Val Pro Val Val Ala Ser Thr Gly Gly Leu Val Asp Thr Val Lys	
485 490 495	
gag ggc gtc acc ggc ttc cac atg ggc gcc ctg aac ccc gac aag ctg	1536
Glu Gly Val Thr Gly Phe His Met Gly Ala Leu Asn Pro Asp Lys Leu	
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Asp Glu Ala Asp Ala Asp Ala Leu Ala Ala Thr Val Arg Arg Ala Ser	
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Glu Val Phe Ala Gly Gly Arg Tyr Pro Glu Met Val Ala Asn Cys Ile	
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agc cag gac ctg tcc tgg tcc aag ccc gcc cag aag tgg gag ggc ctg	1680
Ser Gln Asp Leu Ser Trp Ser Lys Pro Ala Gln Lys Trp Glu Gly Leu	
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ctg gag gag gtg gtg tac ggc aag ggc ggc gtg gcc acc gcc aag aag	1728
Leu Glu Glu Val Val Tyr Gly Lys Gly Gly Val Ala Thr Ala Lys Lys	
565 570 575	
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Glu Glu Ile Lys Val Pro Val Ala Glu Lys Ile Pro Gly Asp Leu Pro	
580 585 590	

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Ala Val Ser Tyr Ala Pro Asn Thr Leu Lys Pro Val Ser Ala Ser Val  
595 600 605

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Glu Gly Asn Gly Ala Ala Ala Pro Lys Val Gly Thr Thr Ala Pro Ala  
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Met Gly Ala Trp Arg Ala Thr Thr Pro Ser Gly Pro Ser Pro Ala Ala  
625 630 635 640

gcc acc ccc aag gtg acc acc tac aag ccc gcc ctg ccc gcc acc gcc 1968  
Ala Thr Pro Lys Val Thr Thr Tyr Lys Pro Ala Leu Pro Ala Thr Ala  
645 650 655

aag ccc aag acc gct ggc ctc aag ctg gcc ggt gag gcc tcc acc acc 2016  
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660 665 670

tcg acc tgc gag aac ggc gct gcc tcc aac ggc aac ggc aac ggt gcc 2064  
Ser Thr Ser Glu Asn Gly Ala Ala Ser Asn Gly Asn Gly Asn Gly Ala  
675 680 685

tcg gcc tcc aag acc tcg gct gcc aag ccc ctg gtc tcc gcc gcc acc 2112  
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<211> 708

<212> PRT

<213> Artificial sequence

<223> Description of the artificial sequence: fragment of the complete sequence of cDNA coding for the GBSSI of *Chlamydomonas reinhardtii*

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20 25 30

Arg Glu Leu Ala Arg Gly Ser Ala Arg Lys Ser Thr Ser Arg Ser Ala  
35 40 45

Val Thr Gly Ala Thr Gly Ala Thr Cys Ala Leu Asp Ile Val Met Val  
50 55 60

Ala Ala Glu Val Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val  
65 70 75 80

Thr Gly Gly Leu Pro Ile Glu Leu Val Lys Arg Gly His Arg Val Met  
85 90 95

Thr	Ile	Ala	Pro	Arg	Tyr	Asp	Gln	Tyr	Ala	Asp	Ala	Trp	Asp	Thr	Ser	100	105	110	
Val	Val	Val	Asp	Ile	Met	Gly	Glu	Lys	Val	Arg	Tyr	Phe	His	Ser	Ile	115	120	125	
Lys	Lys	Gly	Val	His	Arg	Val	Trp	Ile	Asp	His	Pro	Trp	Phe	Leu	Ala	130	135	140	
Lys	Val	Trp	Gly	Lys	Thr	Gly	Ser	Lys	Leu	Tyr	Gly	Pro	Arg	Ser	Gly	145	150	155	160
Ala	Asp	Tyr	Leu	Asp	Asn	His	Lys	Arg	Phe	Ala	Leu	Phe	Cys	Lys	Ala	165	170	175	
Ala	Ile	Glu	Ala	Ala	Arg	Val	Leu	Pro	Phe	Gly	Pro	Gly	Glu	Asp	Cys	180	185	190	
Val	Phe	Val	Ala	Asn	Asp	Trp	His	Ser	Ala	Leu	Val	Pro	Val	Leu	Leu	195	200	205	
Lys	Asp	Glu	Tyr	Gln	Pro	Lys	Gly	Gln	Phe	Thr	Lys	Ala	Lys	Ser	Val	210	215	220	
Leu	Ala	Ile	His	Asn	Ile	Ala	Phe	Gln	Gly	Arg	Met	Trp	Glu	Glu	Ala	225	230	235	240
Phe	Lys	Asp	Thr	Lys	Leu	Pro	Gln	Ala	Ala	Phe	Asp	Lys	Leu	Ala	Phe	245	250	255	
Ser	Asp	Gly	Tyr	Ala	Lys	Val	Tyr	Thr	Glu	Ala	Thr	Pro	Met	Glu	Glu	260	265	270	
Asp	Glu	Lys	Pro	Pro	Leu	Thr	Gly	Lys	Thr	Tyr	Lys	Lys	Ile	Asn	Trp	275	280	285	
Leu	Lys	Gly	Gly	Ile	Ile	Ala	Ala	Asp	Lys	Leu	Val	Thr	Val	Ser	Pro	290	295	300	
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Asp	Thr	Val	Ile	Arg	Ala	Lys	Gly	Ile	Glu	Gly	Ile	Val	Asn	Gly	Met	325	330	335	
Asp	Ile	Glu	Glu	Trp	Asn	Pro	Lys	Thr	Asp	Lys	Phe	Leu	Ser	Ala	Pro	340	345	350	
Tyr	Asp	Gln	Asn	Ser	Val	Tyr	Ala	Gly	Lys	Ala	Ala	Ala	Lys	Glu	Ala	355	360	365	
Leu	Gln	Ala	Glu	Leu	Gly	Leu	Pro	Val	Asp	Pro	Thr	Ala	Pro	Leu	Phe	370	375	380	
Ala	Phe	Ile	Gly	Arg	Leu	Glu	Glu	Gln	Lys	Gly	Val	Asp	Ile	Ile	Leu	385	390	395	400
Ala	Ala	Leu	Pro	Lys	Ile	Leu	Ala	Thr	Pro	Lys	Val	Gln	Ile	Ala	Ile	405	410	415	

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 Thr Lys Tyr Lys Gly Arg Ala Lys Gly Val Val Lys Phe Ser Ala Pro  
 435 440 445  
 Leu Ala His Met Leu Thr Ala Gly Ala Asp Phe Met Leu Val Pro Ser  
 450 455 460  
 Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu His Ala Met His Tyr Gly  
 465 470 475 480  
 Thr Val Pro Val Val Ala Ser Thr Gly Gly Leu Val Asp Thr Val Lys  
 485 490 495  
 Glu Gly Val Thr Gly Phe His Met Gly Ala Leu Asn Pro Asp Lys Leu  
 500 505 510  
 Asp Glu Ala Asp Ala Asp Ala Leu Ala Ala Thr Val Arg Arg Ala Ser  
 515 520 525  
 Glu Val Phe Ala Gly Gly Arg Tyr Pro Glu Met Val Ala Asn Cys Ile  
 530 535 540  
 Ser Gln Asp Leu Ser Trp Ser Lys Pro Ala Gln Lys Trp Glu Gly Leu  
 545 550 555 560  
 Leu Glu Glu Val Val Tyr Gly Lys Gly Gly Val Ala Thr Ala Lys Lys  
 565 570 575  
 Glu Glu Ile Lys Val Pro Val Ala Glu Lys Ile Pro Gly Asp Leu Pro  
 580 585 590  
 Ala Val Ser Tyr Ala Pro Asn Thr Leu Lys Pro Val Ser Ala Ser Val  
 595 600 605  
 Glu Gly Asn Gly Ala Ala Ala Pro Lys Val Gly Thr Thr Ala Pro Ala  
 610 615 620  
 Met Gly Ala Trp Arg Ala Thr Thr Pro Ser Gly Pro Ser Pro Ala Ala  
 625 630 635 640  
 Ala Thr Pro Lys Val Thr Thr Tyr Lys Pro Ala Leu Pro Ala Thr Ala  
 645 650 655  
 Lys Pro Lys Thr Ala Gly Leu Lys Leu Ala Gly Glu Ala Ser Thr Thr  
 660 665 670  
 Ser Thr Ser Glu Asn Gly Ala Ala Ser Asn Gly Asn Gly Asn Gly Ala  
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 Arg Lys Ser Ala  
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<210> 4  
 <211> 1953  
 <212> DNA  
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: fragment  
 of the complete cDNA coding for the GBSSI of  
*Chlamydomonas reinhardtii* and coding for the mature GBSSI  
 protein.

<220>

<221> CDS

<222> (1)..(1953)

<400> 4

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Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val	
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aag cgc ggc cac cgc gtc atg acc att gcc cct cgc tac gac cag tac	144
Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr	
35 40 45	
gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag	192
Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys	
50 55 60	
gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att	240
Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile	
65 70 75 80	
gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag	288
Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys	
85 90 95	
ctg tac ggc ccc cgc tcc ggc gct gac tac ctg gac aac cac aag cgc	336
Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg	
100 105 110	
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Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro	
115 120 125	
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Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser	
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Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln	
145 150 155 160	
ttc acc aag gcc aag tcg gtg ctg gct atc cac aac atc gcc ttc cag	528
Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln	
165 170 175	



ggc cgc atg tgg gag gag gct ttc aag gac acg aag ctg ccc cag gcc	576
Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala	
180 185 190	
gcc ttt gac aag ctg gcc ttc tcg gac ggc tat gcc aag gtt tac act	624
Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr	
195 200 205	
gag gcc acc ccc atg gag gag gac gag aag ccc ccg ctg acg gga aag	672
Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys	
210 215 220	
acc tac aag aag atc aac tgg ctg aag ggt ggc att atc gcc gcc gac	720
Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp	
225 230 235 240	
aag ctg gtg act gtg tcg ccc aac tac gcg acc gag atc gct gcc gat	768
Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp	
245 250 255	
gcc gcc ggc ggt gtg gag ctg gac acc gtc atc cgc gcc aag ggc att	816
Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile	
260 265 270	
gag ggc att gtg aac ggc atg gac att gag gag tgg aac ccc aag acc	864
Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr	
275 280 285	
gac aag ttc ctg tct gcg ccc tac gac cag aac agc gtc tac gcc ggc	912
Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly	
290 295 300	
aag gcc gcc gcc aag gag gcc ctg cag gcc gag ctg ggc ctg cct gtg	960
Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val	
305 310 315 320	
gac ccc acc gcc ccc ctg ttc gcc ttc atc ggc cgc ctg gag gag cag	1008
Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln	
325 330 335	
aag ggt gtg gac atc atc ctg gcc gcc ctg ccc aag atc ctg gcc acc	1056
Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr	
340 345 350	
ccc aag gtg cag atc gcc atc ctg ggt acc ggc aag gcc gcc tac gag	1104
Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu	
355 360 365	
aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc	1152
Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly	
370 375 380	
gtg gtc aag ttc tcg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc	1200
Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala	
385 390 395 400	
gac ttc atg ctg gtg ccc tcg cgc ttc gag ccc tgc ggc ctg atc cag	1248
Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln	
405 410 415	

ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc	1296
Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly	
420 425 430	
ggc ctg gtc gac acc gtc aag gag ggc gtc acc ggc ttc cac atg ggc	1344
Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly	
435 440 445	
gcc ctg aac ccc gac aag ctg gac gag gct gac gcc gac gcc ctg gcc	1392
Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala	
450 455 460	
gcc acc gtg cgc cgt gcc agc gag gtg ttt gcg ggc ggc cgc tac ccc	1440
Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro	
465 470 475 480	
gag atg gtg gcc aac tgc atc agc cag gac ctg tcc tgg tcc aag ccc	1488
Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro	
485 490 495	
gcc cag aag tgg gag ggc ctg ctg gag gag gtg gtg tac ggc aag ggc	1536
Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly	
500 505 510	
ggc gtg gcc acc gcc aag aag gag gag atc aag gtg ccc gtt gcc gag	1584
Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu	
515 520 525	
aag atc ccc ggc gac ctg ccc gcc gtg tcc tac gcc ccc aac acc ctg	1632
Lys Ile Pro Gly Asp Leu Pro Ala Val Ser Tyr Ala Pro Asn Thr Leu	
530 535 540	
aag ccc gtg tcc gcc tcc gtg gag ggc aac ggc gcc gcc gcg ccc aag	1680
Lys Pro Val Ser Ala Ser Val Glu Gly Asn Gly Ala Ala Ala Pro Lys	
545 550 555 560	
gtc ggc acc acc gcc ccc gcc atg ggc gcg tgg cgc gcg acc acc ccc	1728
Val Gly Thr Thr Ala Pro Ala Met Gly Ala Trp Arg Ala Thr Thr Pro	
565 570 575	
tcg ggc ccc tcg ccc gcc gcc gcc acc ccc aag gtg acc acc tac aag	1776
Ser Gly Pro Ser Pro Ala Ala Ala Thr Pro Lys Val Thr Thr Tyr Lys	
580 585 590	
ccc gcc ctg ccc gcc acc gcc aag ccc aag acc gct ggc ctc aag ctg	1824
Pro Ala Leu Pro Ala Thr Ala Lys Pro Lys Thr Ala Gly Leu Lys Leu	
595 600 605	
gcc ggt gag gcc tcc acc acc tcg acc tcg gag aac ggc gct gcc tcc	1872
Ala Gly Glu Ala Ser Thr Thr Ser Thr Ser Glu Asn Gly Ala Ala Ser	
610 615 620	
aac ggc aac ggc aac ggt gcc tcg gcc tcc aag acc tcg gct gcc aag	1920
Asn Gly Asn Gly Asn Gly Ala Ser Ala Ser Lys Thr Ser Ala Ala Lys	
625 630 635 640	
ccc ctg gtc tcc gcc gcc acc cgc aag tcc gcc	1953
Pro Leu Val Ser Ala Ala Thr Arg Lys Ser Ala	
645 650	

<210> 5  
 <211> 651  
 <212> PRT  
 <213> Artificial sequence  
 <223> Description of the artificial sequence: fragment  
 of the complete cDNA coding for the GBSSI  
 of *Chlamydomonas reinhardtii* and coding for the mature  
 GBSSI protein

<400> 5

Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys  
 1 5 10 15

Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
 20 25 30

Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
 35 40 45

Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
 50 55 60

Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
 65 70 75 80

Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
 85 90 95

Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
 100 105 110

Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro  
 115 120 125

Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser  
 130 135 140

Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln  
 145 150 155 160

Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln  
 165 170 175

Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala  
 180 185 190

Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr  
 195 200 205

Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys  
 210 215 220

Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp  
 225 230 235 240

Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp  
 245 250 255

Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile  
 260 265 270

Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr  
 275 280 285  
 Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly  
 290 295 300  
 Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val  
 305 310 315 320  
 Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln  
 325 330 335  
 Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr  
 340 345 350  
 Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu  
 355 360 365  
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly  
 370 375 380  
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala  
 385 390 395 400  
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln  
 405 410 415  
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly  
 420 425 430  
 Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly  
 435 440 445  
 Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala  
 450 455 460  
 Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro  
 465 470 475 480  
 Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro  
 485 490 495  
 Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly  
 500 505 510  
 Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu  
 515 520 525  
 Lys Ile Pro Gly Asp Leu Pro Ala Val Ser Tyr Ala Pro Asn Thr Leu  
 530 535 540  
 Lys Pro Val Ser Ala Ser Val Glu Gly Asn Gly Ala Ala Ala Pro Lys  
 545 550 555 560  
 Val Gly Thr Thr Ala Pro Ala Met Gly Ala Trp Arg Ala Thr Thr Pro  
 565 570 575  
 Ser Gly Pro Ser Pro Ala Ala Ala Thr Pro Lys Val Thr Thr Tyr Lys  
 580 585 590

Pro Ala Leu Pro Ala Thr Ala Lys Pro Lys Thr Ala Gly Leu Lys Leu  
595 600 605

Ala Gly Glu Ala Ser Thr Thr Ser Thr Ser Glu Asn Gly Ala Ala Ser  
610 615 620

Asn Gly Asn Gly Asn Gly Ala Ser Ala Ser Lys Thr Ser Ala Ala Lys  
625 630 635 640

Pro Leu Val Ser Ala Ala Thr Arg Lys Ser Ala  
645 650

<210> 6

<211> 1314

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fragment  
of the complete cDNA coding for the GBSSI  
of *Chlamydomonas reinhardtii*

<220>

<221> CDS

<222> (1)..(1314)

<400> 6

gcg ctg gac atc gtg atg gtt gct gct gag gtc gcc cct tgg tcc aag 48  
Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys  
1 5 10 15

acg ggc ggc ctg ggc gat gtg act ggt ggc ctg cct att gag ctg gtc 96  
Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
20 25 30

aag cgc ggc cac cgc gtc atg acc att gcc cct cgc tac gac cag tac 144  
Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
35 40 45

gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag 192  
Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
50 55 60

gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att 240  
Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
65 70 75 80

gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag 288  
Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
85 90 95

ctg tac ggc ccc cgc tcc ggc gct gac tac ctg gac aac cac aag cgc 336  
Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
100 105 110

ttc gcc ctg ttc tgc aag gcc gct att gag gct gcc cgc gtg ctg ccc 384  
Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro

115	120	125	
ttc ggc ccc ggc gag gac	tgc gtc ttc gtg gcc	aac gac tgg cac tcc	432
Phe Gly Pro Gly Glu Asp	Cys Val Phe Val Ala	Asn Asp Trp His Ser	
130	135	140	
gcc ctg gtg ccc gtc ctg	ctg aag gac gag tac	cag ccc aag ggc cag	480
Ala Leu Val Pro Val Leu	Leu Lys Asp Glu Tyr	Gln Pro Lys Gly Gln	
145	150	155 160	
ttc acc aag gcc aag tcg	gtg ctg gct atc cac	aac atc gcc ttc cag	528
Phe Thr Lys Ala Lys Ser	Val Leu Ala Ile His	Asn Ile Ala Phe Gln	
165	170	175	
ggc cgc atg tgg gag gag	gct ttc aag gac acg	aag ctg ccc cag gcc	576
Gly Arg Met Trp Glu Glu	Ala Phe Lys Asp Thr	Lys Leu Pro Gln Ala	
180	185	190	
gcc ttt gac aag ctg gcc	ttc tcg gac ggc tat	gcc aag gtt tac act	624
Ala Phe Asp Lys Leu Ala	Phe Ser Asp Gly Tyr	Ala Lys Val Tyr Thr	
195	200	205	
gag gcc acc ccc atg gag	gag gac gag aag ccc	ccg ctg acg gga aag	672
Glu Ala Thr Pro Met Glu	Glu Asp Glu Lys Pro	Pro Leu Thr Gly Lys	
210	215	220	
acc tac aag aag atc aac	tgg ctg aag ggt ggc	att atc gcc gcc gac	720
Thr Tyr Lys Lys Ile Asn	Trp Leu Lys Gly Gly	Ile Ile Ala Ala Asp	
225	230	235 240	
aag ctg gtg act gtg tcg	ccc aac tac gcg acc	gag atc gct gcc gat	768
Lys Leu Val Thr Val Ser	Pro Asn Tyr Ala Thr	Glu Ile Ala Ala Asp	
245	250	255	
gcc gcc ggc ggt gtg gag	ctg gac acc gtc atc	cgc gcc aag ggc att	816
Ala Ala Gly Gly Val Glu	Leu Asp Thr Val Ile	Arg Ala Lys Gly Ile	
260	265	270	
gag ggc att gtg aac ggc	atg gac att gag gag	tgg aac ccc aag acc	864
Glu Gly Ile Val Asn Gly	Met Asp Ile Glu Glu	Trp Asn Pro Lys Thr	
275	280	285	
gac aag ttc ctg tct gcg	ccc tac gac cag aac	agc gtc tac gcc ggc	912
Asp Lys Phe Leu Ser Ala	Pro Tyr Asp Gln Asn	Ser Val Tyr Ala Gly	
290	295	300	
aag gcc gcc gcc aag gag	gcc ctg cag gcc gag	ctg ggc ctg cct gtg	960
Lys Ala Ala Ala Lys Glu	Ala Leu Gln Ala Glu	Leu Gly Leu Pro Val	
305	310	315 320	
gac ccc acc gcc ccc ctg	ttc gcc ttc atc ggc	cgc ctg gag gag cag	1008
Asp Pro Thr Ala Pro Leu	Phe Ala Phe Ile Gly	Arg Leu Glu Glu Gln	
325	330	335	
aag ggt gtg gac atc atc	ctg gcc gcc ctg ccc	aag atc ctg gcc acc	1056
Lys Gly Val Asp Ile Ile	Leu Ala Ala Leu Pro	Lys Ile Leu Ala Thr	
340	345	350	
ccc aag gtg cag atc gcc	atc ctg ggt acc ggc	aag gcc gcc tac gag	1104
Pro Lys Val Gln Ile Ala	Ile Leu Gly Thr Gly	Lys Ala Ala Tyr Glu	
355	360	365	

aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc 1152  
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly  
 370 375 380

gtg gtc aag ttc tcg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc 1200  
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala  
 385 390 395 400

gac ttc atg ctg gtg ccc tcg cgc ttc gag ccc tgc ggc ctg atc cag 1248  
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln  
 405 410 415

ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc 1296  
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly  
 420 425 430

ggc ctg gtc gac acc gtc 1314  
 Gly Leu Val Asp Thr Val  
 435

<210> 7

<211> 438

<212> PRT

<213> Artificial sequence

<223> Description of the artificial sequence: fragment  
 of the complete cDNA coding for the GBSSI  
 of Chlamydomonas reinhardtii

<400> 7

Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys  
 1 5 10 15

Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val  
 20 25 30

Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr  
 35 40 45

Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys  
 50 55 60

Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile  
 65 70 75 80

Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys  
 85 90 95

Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg  
 100 105 110

Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro  
 115 120 125

Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser  
 130 135 140

Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln  
 145 150 155 160

Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln  
 165 170 175  
 Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala  
 180 185 190  
 Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr  
 195 200 205  
 Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys  
 210 215 220  
 Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp  
 225 230 235 240  
 Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp  
 245 250 255  
 Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile  
 260 265 270  
 Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr  
 275 280 285  
 Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly  
 290 295 300  
 Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val  
 305 310 315 320  
 Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln  
 325 330 335  
 Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr  
 340 345 350  
 Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu  
 355 360 365  
 Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly  
 370 375 380  
 Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala  
 385 390 395 400  
 Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln  
 405 410 415  
 Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly  
 420 425 430  
 Gly Leu Val Asp Thr Val  
 435

&lt;210&gt; 8

&lt;211&gt; 1593

&lt;212&gt; DNA



<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fragment  
of the complete cDNA coding for the GBSSI  
of *Chlamydomonas reinhardtii*

<220>

<221> CDS

<222> (1)..(1593)

<400> 8

gcg ctg gac atc gtg atg gtt gct gct gag gtc gcc cct tgg tcc aag	48
Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys	
1 5 10 15	
acg ggc ggc ctg ggc gat gtg act ggt ggc ctg cct att gag ctg gtc	96
Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val	
20 25 30	
aag cgc ggc cac cgc gtc atg acc att gcc cct cgc tac gac cag tac	144
Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr	
35 40 45	
gct gac gcc tgg gac acc tcg gtg gtc gtg gac atc atg ggc gag aag	192
Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys	
50 55 60	
gtc cgc tac ttc cac tcc atc aag aag ggc gtg cac cgc gtg tgg att	240
Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile	
65 70 75 80	
gac cac ccc tgg ttc ctg gcc aag gtc tgg ggc aag acc ggc tcc aag	288
Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys	
85 90 95	
ctg tac ggc ccc cgc tcc ggc gct gac tac ctg gac aac cac aag cgc	336
Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg	
100 105 110	
ttc gcc ctg ttc tgc aag gcc gct att gag gct gcc cgc gtg ctg ccc	384
Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro	
115 120 125	
ttc ggc ccc ggc gag gac tgc gtc ttc gtg gcc aac gac tgg cac tcc	432
Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser	
130 135 140	
gcc ctg gtg ccc gtc ctg ctg aag gac gag tac cag ccc aag ggc cag	480
Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln	
145 150 155 160	
ttc acc aag gcc aag tcg gtg ctg gct atc cac aac atc gcc ttc cag	528
Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln	
165 170 175	
ggc cgc atg tgg gag gag gct ttc aag gac acg aag ctg ccc cag gcc	576
Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala	
180 185 190	
gcc ttt gac aag ctg gcc ttc tcg gac ggc tat gcc aag gtt tac act	624

Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr	
195 200 205	
gag gcc acc ccc atg gag gag gac gag aag ccc ccg ctg acg gga aag	672
Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys	
210 215 220	
acc tac aag aag atc aac tgg ctg aag ggt ggc att atc gcc gcc gac	720
Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp	
225 230 235 240	
aag ctg gtg act gtg tgg ccc aac tac gcg acc gag atc gct gcc gat	768
Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp	
245 250 255	
gcc gcc ggc ggt gtg gag ctg gac acc gtc atc cgc gcc aag ggc att	816
Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile	
260 265 270	
gag ggc att gtg aac ggc atg gac att gag gag tgg aac ccc aag acc	864
Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr	
275 280 285	
gac aag ttc ctg tct gcg ccc tac gac cag aac agc gtc tac gcc ggc	912
Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly	
290 295 300	
aag gcc gcc gcc aag gag gcc ctg cag gcc gag ctg ggc ctg cct gtg	960
Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val	
305 310 315 320	
gac ccc acc gcc ccc ctg ttc gcc ttc atc ggc cgc ctg gag gag cag	1008
Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln,	
325 330 335	
aag ggt gtg gac atc atc ctg gcc gcc ctg ccc aag atc ctg gcc acc	1056
Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr	
340 345 350	
ccc aag gtg cag atc gcc atc ctg ggt acc ggc aag gcc gcc tac gag	1104
Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu	
355 360 365	
aag ctg gtg aac gcc atc ggc acc aag tac aag ggc cgc gcc aag ggc	1152
Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly	
370 375 380	
gtg gtc aag ttc tgg gcg ccc ctg gcg cac atg ctc acc gcc ggc gcc	1200
Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala	
385 390 395 400	
gac ttc atg ctg gtg ccc tgg cgc ttc gag ccc tgc ggc ctg atc cag	1248
Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln	
405 410 415	
ctg cac gcc atg cac tac ggt acc gtg ccc gtg gta gcc tcc acc ggc	1296
Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly	
420 425 430	
ggc ctg gtc gac acc gtc aag gag ggc gtc acc ggc ttc cac atg ggc	1344
Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly	

435					440					445						
gcc	ctg	aac	ccc	gac	aag	ctg	gac	gag	gct	gac	gcc	gac	gcc	ctg	gcc	1392
Ala	Leu	Asn	Pro	Asp	Lys	Leu	Asp	Glu	Ala	Asp	Ala	Asp	Ala	Leu	Ala	
450					455					460						
gcc	acc	gtg	cgc	cgt	gcc	agc	gag	gtg	ttt	gcg	ggc	ggc	cgc	tac	ccc	1440
Ala	Thr	Val	Arg	Arg	Ala	Ser	Glu	Val	Phe	Ala	Gly	Gly	Arg	Tyr	Pro	
465					470					475					480	
gag	atg	gtg	gcc	aac	tgc	atc	agc	cag	gac	ctg	tcc	tgg	tcc	aag	ccc	1488
Glu	Met	Val	Ala	Asn	Cys	Ile	Ser	Gln	Asp	Leu	Ser	Trp	Ser	Lys	Pro	
485					490					495						
gcc	cag	aag	tgg	gag	ggc	ctg	ctg	gag	gag	gtg	gtg	tac	ggc	aag	ggc	1536
Ala	Gln	Lys	Trp	Glu	Gly	Leu	Leu	Glu	Glu	Val	Val	Tyr	Gly	Lys	Gly	
500					505					510						
ggc	gtg	gcc	acc	gcc	aag	aag	gag	gag	atc	aag	gtg	ccc	gtt	gcc	gag	1584
Gly	Val	Ala	Thr	Ala	Lys	Lys	Glu	Glu	Ile	Lys	Val	Pro	Val	Ala	Glu	
515					520					525						
aag	atc	ccc														1593
Lys	Ile	Pro														
530																

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<210> 9
<211> 531
<212> PRT
<213> Artificial sequence
<223> Description of the artificial sequence: fragment
      of the complete cDNA coding for the GBSSI
      of Chlamydomonas reinhardtii
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<400> 9
Ala Leu Asp Ile Val Met Val Ala Ala Glu Val Ala Pro Trp Ser Lys
  1                      5                      10                      15

Thr Gly Gly Leu Gly Asp Val Thr Gly Gly Leu Pro Ile Glu Leu Val
                20                      25                      30

Lys Arg Gly His Arg Val Met Thr Ile Ala Pro Arg Tyr Asp Gln Tyr
      35                      40                      45

Ala Asp Ala Trp Asp Thr Ser Val Val Val Asp Ile Met Gly Glu Lys
  50                      55                      60

Val Arg Tyr Phe His Ser Ile Lys Lys Gly Val His Arg Val Trp Ile
  65                      70                      75                      80

Asp His Pro Trp Phe Leu Ala Lys Val Trp Gly Lys Thr Gly Ser Lys
                85                      90                      95

Leu Tyr Gly Pro Arg Ser Gly Ala Asp Tyr Leu Asp Asn His Lys Arg
      100                      105                      110

Phe Ala Leu Phe Cys Lys Ala Ala Ile Glu Ala Ala Arg Val Leu Pro
     115                      120                      125

Phe Gly Pro Gly Glu Asp Cys Val Phe Val Ala Asn Asp Trp His Ser

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130	135	140
Ala Leu Val Pro Val Leu Leu Lys Asp Glu Tyr Gln Pro Lys Gly Gln 145	150	155 160
Phe Thr Lys Ala Lys Ser Val Leu Ala Ile His Asn Ile Ala Phe Gln 165	170	175
Gly Arg Met Trp Glu Glu Ala Phe Lys Asp Thr Lys Leu Pro Gln Ala 180	185	190
Ala Phe Asp Lys Leu Ala Phe Ser Asp Gly Tyr Ala Lys Val Tyr Thr 195	200	205
Glu Ala Thr Pro Met Glu Glu Asp Glu Lys Pro Pro Leu Thr Gly Lys 210	215	220
Thr Tyr Lys Lys Ile Asn Trp Leu Lys Gly Gly Ile Ile Ala Ala Asp 225	230	235 240
Lys Leu Val Thr Val Ser Pro Asn Tyr Ala Thr Glu Ile Ala Ala Asp 245	250	255
Ala Ala Gly Gly Val Glu Leu Asp Thr Val Ile Arg Ala Lys Gly Ile 260	265	270
Glu Gly Ile Val Asn Gly Met Asp Ile Glu Glu Trp Asn Pro Lys Thr 275	280	285
Asp Lys Phe Leu Ser Ala Pro Tyr Asp Gln Asn Ser Val Tyr Ala Gly 290	295	300
Lys Ala Ala Ala Lys Glu Ala Leu Gln Ala Glu Leu Gly Leu Pro Val 305	310	315 320
Asp Pro Thr Ala Pro Leu Phe Ala Phe Ile Gly Arg Leu Glu Glu Gln 325	330	335
Lys Gly Val Asp Ile Ile Leu Ala Ala Leu Pro Lys Ile Leu Ala Thr 340	345	350
Pro Lys Val Gln Ile Ala Ile Leu Gly Thr Gly Lys Ala Ala Tyr Glu 355	360	365
Lys Leu Val Asn Ala Ile Gly Thr Lys Tyr Lys Gly Arg Ala Lys Gly 370	375	380
Val Val Lys Phe Ser Ala Pro Leu Ala His Met Leu Thr Ala Gly Ala 385	390	395 400
Asp Phe Met Leu Val Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln 405	410	415
Leu His Ala Met His Tyr Gly Thr Val Pro Val Val Ala Ser Thr Gly 420	425	430
Gly Leu Val Asp Thr Val Lys Glu Gly Val Thr Gly Phe His Met Gly 435	440	445
Ala Leu Asn Pro Asp Lys Leu Asp Glu Ala Asp Ala Asp Ala Leu Ala 450	455	460

Ala Thr Val Arg Arg Ala Ser Glu Val Phe Ala Gly Gly Arg Tyr Pro  
 465 470 475 480

Glu Met Val Ala Asn Cys Ile Ser Gln Asp Leu Ser Trp Ser Lys Pro  
 485 490 495

Ala Gln Lys Trp Glu Gly Leu Leu Glu Glu Val Val Tyr Gly Lys Gly  
 500 505 510

Gly Val Ala Thr Ala Lys Lys Glu Glu Ile Lys Val Pro Val Ala Glu  
 515 520 525

Lys Ile Pro  
 530

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